

50c

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/521,748
Source: PC/10
Date Processed by STIC: 11/17/06

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 01/17/2006

PATENT APPLICATION: US/10/521,748

TIME: 11:29:39

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\01172006\J521748.raw

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3 <110> APPLICANT: Cellzome AG
5 <120> TITLE OF INVENTION: Protein complexes of the TIP60 transcriptional
6   activator protein as well as components, fragments
7   and derivatives thereof and methods for using the same
9 <130> FILE REFERENCE: Protein complexes of the TIP60 transcriptional
W--> 10 activator protein as well as components, fragments and
W--> 11 derivatives thereof and methods for using the same
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/521,748
C--> 13 <141> CURRENT FILING DATE: 2005-01-19
13 <150> PRIOR APPLICATION NUMBER: EP02016110.5
14 <151> PRIOR FILING DATE: 2002-07-19
16 <150> PRIOR APPLICATION NUMBER: EP03101321.2
17 <151> PRIOR FILING DATE: 2003-05-12
19 <160> NUMBER OF SEQ ID NOS: 18
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 919
25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapiens
28 <400> SEQUENCE: 1
30 Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
31 1 5 10 15
34 Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
35 20 25 30
38 Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
39 35 40 45
42 Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln
43 50 55 60
46 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Thr
47 65 70 75 80
50 Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro Gln
51 85 90 95
54 Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln
55 100 105 110
58 Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly
59 115 120 125
62 Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro
63 130 135 140
66 Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser
67 145 150 155 160
70 Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser
71 165 170 175
74 Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu

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75          180          185          190
78 Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg
79          195          200          205
82 Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu
83          210          215          220
86 Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala
87 225          230          235          240
90 Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser
91          245          250          255
94 Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly
95          260          265          270
98 Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys
99          275          280          285
102 Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr
103          290          295          300
106 Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu Glu Gly
107 305          310          315          320
110 Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser Gly Thr
111          325          330          335
114 Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp
115          340          345          350
118 Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro Leu Ala
119          355          360          365
122 Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro His Pro His Ala Arg
123          370          375          380
126 Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala
127 385          390          395          400
130 Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Ala Gly
131          405          410          415
134 Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser Ser Ser
135          420          425          430
138 Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Cys
139          435          440          445
142 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
143          450          455          460
146 Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala Val Ala Pro Tyr
147 465          470          475          480
150 Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp Phe
151          485          490          495
154 Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val Pro
155          500          505          510
158 Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met Asp
159          515          520          525
162 Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Glu Thr Ala Arg Asp
163          530          535          540
166 His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu
167 545          550          555          560
170 Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys
171          565          570          575

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174 Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys
175          580          585          590
178 Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg
179          595          600          605
182 Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met
183          610          615          620
186 Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln
187 625          630          635          640
190 Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr
191          645          650          655
194 Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile
195          660          665          670
198 Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly
199          675          680          685
202 His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu
203          690          695          700
206 Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys
207 705          710          715          720
210 Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val
211          725          730          735
214 Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg
215          740          745          750
218 Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu
219          755          760          765
222 Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys
223          770          775          780
226 Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr
227 785          790          795          800
230 Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile
231          805          810          815
234 Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met
235          820          825          830
238 Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn
239          835          840          845
242 Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp
243          850          855          860
246 Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu
247 865          870          875          880
250 Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala
251          885          890          895
254 Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys
255          900          905          910
258 Pro Ile Tyr Phe His Thr Gln
259          915
262 <210> SEQ ID NO: 2
263 <211> LENGTH: 375
264 <212> TYPE: PRT
265 <213> ORGANISM: Homo sapiens
267 <400> SEQUENCE: 2

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269 Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn Gly Ser Gly Met
270 1 5 10 15
273 Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
274 20 25 30
277 Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
278 35 40 45
281 Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
282 50 55 60
285 Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
286 65 70 75 80
289 Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
290 85 90 95
293 Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
294 100 105 110
297 Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
298 115 120 125
301 Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
302 130 135 140
305 Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
306 145 150 155 160
309 His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu
310 165 170 175
313 Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile
314 180 185 190
317 Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile
318 195 200 205
321 Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe Glu
322 210 215 220
325 Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr
326 225 230 235 240
329 Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe Arg
330 245 250 255
333 Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys
334 260 265 270
337 Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp
338 275 280 285
341 Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr
342 290 295 300
345 Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu
346 305 310 315 320
349 Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys
350 325 330 335
353 Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe
354 340 345 350
357 Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser
358 355 360 365
361 Ile Val His Arg Lys Cys Phe
362 370 375
365 <210> SEQ ID NO: 3

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Input Set : A:\Sequence Listing.txt

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366 <211> LENGTH: 429

367 <212> TYPE: PRT

368 <213> ORGANISM: Homo sapiens

370 <400> SEQUENCE: 3

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372 Met Ser Gly Gly Val Tyr Gly Gly Asp Glu Val Gly Ala Leu Val Phe
373 1 5 10 15
376 Asp Ile Gly Ser Tyr Thr Val Arg Ala Gly Tyr Ala Gly Glu Asp Cys
377 20 25 30
380 Pro Lys Val Asp Phe Pro Thr Ala Ile Gly Met Val Val Glu Arg Asp
381 35 40 45
384 Asp Gly Ser Thr Leu Met Glu Ile Asp Gly Asp Lys Gly Lys Gln Gly
385 50 55 60
388 Gly Pro Thr Tyr Tyr Ile Asp Thr Asn Ala Leu Arg Val Pro Arg Glu
389 65 70 75 80
392 Asn Met Glu Ala Ile Ser Pro Leu Lys Asn Gly Met Val Glu Asp Trp
393 85 90 95
396 Asp Ser Phe Gln Ala Ile Leu Asp His Thr Tyr Lys Met His Val Lys
397 100 105 110
400 Ser Glu Ala Ser Leu His Pro Val Leu Met Ser Glu Ala Pro Trp Asn
401 115 120 125
404 Thr Arg Ala Lys Arg Glu Lys Leu Thr Glu Leu Met Phe Glu His Tyr
405 130 135 140
408 Asn Ile Pro Ala Phe Phe Leu Cys Lys Thr Ala Val Leu Thr Ala Phe
409 145 150 155 160
412 Ala Asn Gly Arg Ser Thr Gly Leu Ile Leu Asp Ser Gly Ala Thr His
413 165 170 175
416 Thr Thr Ala Ile Pro Val His Asp Gly Tyr Val Leu Gln Gln Gly Ile
417 180 185 190
420 Val Lys Ser Pro Leu Ala Gly Asp Phe Ile Thr Met Gln Cys Arg Glu
421 195 200 205
424 Leu Phe Gln Glu Met Asn Ile Glu Leu Val Pro Pro Tyr Met Ile Ala
425 210 215 220
428 Ser Lys Glu Ala Val Arg Glu Gly Ser Pro Ala Asn Trp Lys Arg Lys
429 225 230 235 240
432 Glu Lys Leu Pro Gln Val Thr Arg Ser Trp His Asn Tyr Met Cys Asn
433 245 250 255
436 Cys Val Ile Gln Asp Phe Gln Ala Ser Val Leu Gln Val Ser Asp Ser
437 260 265 270
440 Thr Tyr Asp Glu Gln Val Ala Ala Gln Met Pro Thr Val His Tyr Glu
441 275 280 285
444 Phe Pro Asn Gly Tyr Asn Cys Asp Phe Gly Ala Glu Arg Leu Lys Ile
445 290 295 300
448 Pro Glu Gly Leu Phe Asp Pro Ser Asn Val Lys Gly Leu Ser Gly Asn
449 305 310 315 320
452 Thr Met Leu Gly Val Ser His Val Val Thr Thr Ser Val Gly Met Cys
453 325 330 335
456 Asp Ile Asp Ile Arg Pro Gly Leu Tyr Gly Ser Val Ile Val Ala Gly
457 340 345 350
460 Gly Asn Thr Leu Ile Gln Ser Phe Thr Asp Arg Leu Asn Arg Glu Leu

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VERIFICATION SUMMARY

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Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\01172006\J521748.raw

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L:11 M:259 W: Allowed number of lines exceeded, <130> FILE REFERENCE:
L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date